

FIG. 1

Hits on Rep

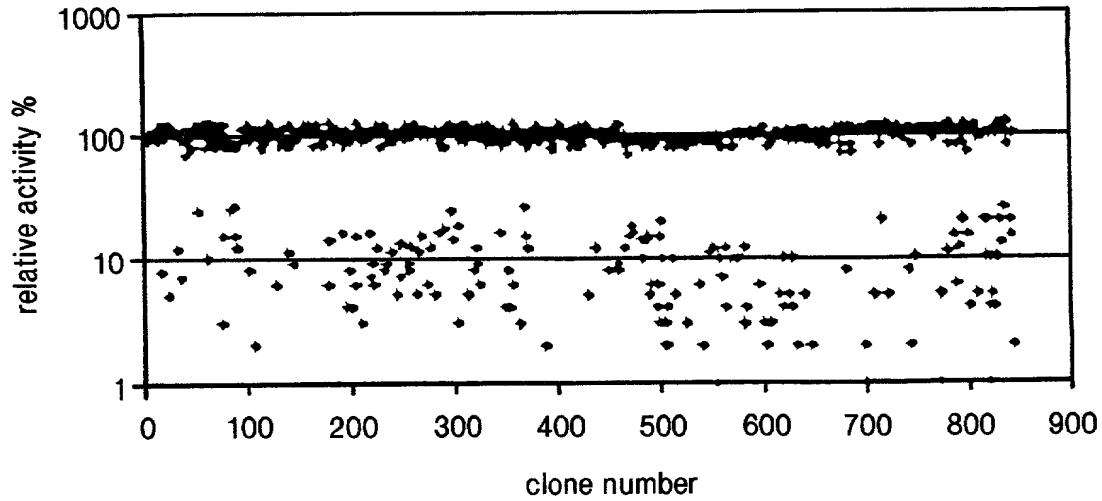


FIG. 2A

Lead positions on Rep

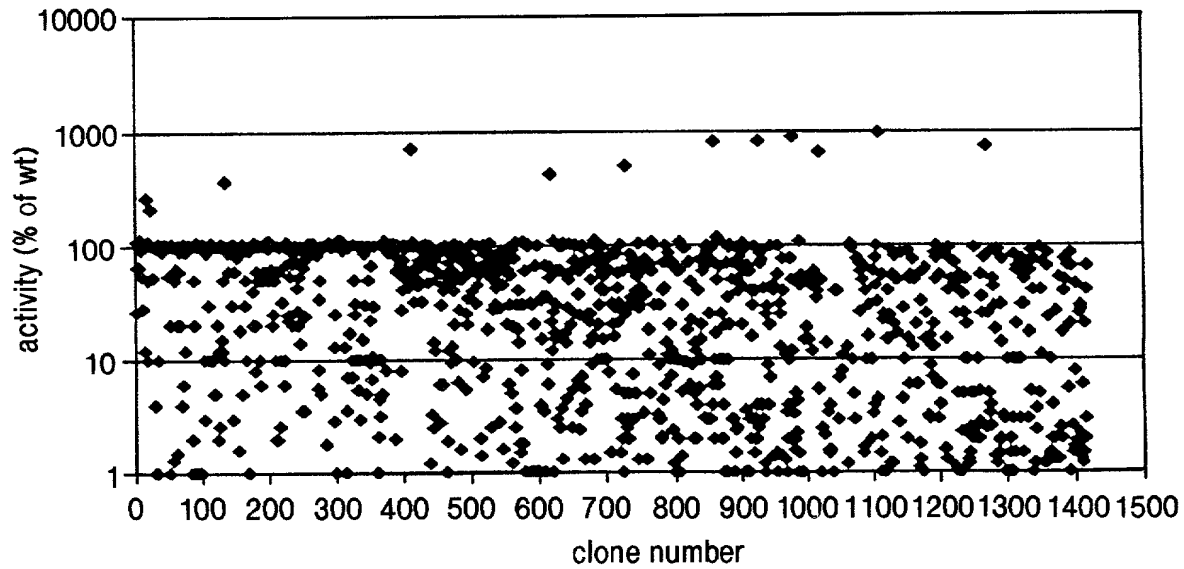


FIG. 2B

10 20 30 40 50 60  
 1 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60  
 2 MPGFYEIVIKVPSDDLDEHLPGISDSFVNWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60  
 3 MPGFYEIVLKVPSDDLDEHLPGISNSFVNWVAEKEWELPPDSMDPNLIEQAPLTVAEKLQ 60  
 4 MPGFYEIVLKVPSDDLDEHLPGISNSFVNWVAEKEWELPPDSMDPNLIEQAPLTVAEKLQ 60  
 5 MPGFYEIVLKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60  
 6 MPGFYEIVIKVPSDDLDEHLPGISDSFVNWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60  
 7 MATFFEIVIRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTVEQPQLTVADRIR 60  
 C M\*\*FYE\*:VP\*D\*\*\*HLPGIS+SFV:WV\*\*\*\*WELPP\*SD\*\*+L\*EQ\*\*LTVA\*\*\*\*  
 70 80 90 100 110 120  
 1 RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLIVETTGVKSMVLGRFLSQIRDKLVQTI 120  
 2 RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLIVETTGVKSMVLGRFLSQIRDKLVQTI 120  
 3 REFLVEWRRVSKAPEALFFVQFEKGETYFHLHLVLIETIGVKSMVVGRYVSQIKEKLVTRI 120  
 4 REFLVEWRRVSKAPEALFFVQFEKGETYFHLHLVLIETIGVKSMVVGRYVSQIKEKLVTRI 120  
 5 REFLVEWRRVSKAPEALFFVQFEKGDYFHLHLIVETGVKSMVVGRYVSQIKEKLVTRI 120  
 6 RDFLTEWRRVSKAPEALFFVQFEKGESYFHMHLVETTGVKSMVLGRFLSQIREKLIQRI 120  
 7 RVFLYEWNKFSKQ-ESKFFVQFEKGEYFHLHTLVETSGISSMVLGRYVSQIRAQLVKV 119  
 C R:FL++W\*\*\*SK\*\*E\*\*FFVQFEKG+:YFH\*H:L+ET:G\*\*SMV:GR::SQI::\*L:::  
 130 140 150 160 170 180  
 1 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWNTNMEEYISACL 180  
 2 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWNTNMEEYISACL 180  
 3 YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWNTNMDQYLSACL 180  
 4 YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWNTNMDQYLSACL 180  
 5 YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWNTNMDQYISACL 180  
 6 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWNTNMEQYLSACL 180  
 7 FQGIPTQINDWVAITKVKK--GGANKVDSGYIPAYLLPKVQPELQAWNTNLDYKLAAL 177  
 C \*\*G:EP:\*\*\*W\*A\*TK\*\*\*\*\*GG\*NKVV:YIP\*YLLPK\*QPELQAWNTN\*:Y:\*A\*L  
 190 200 210 220 230 240  
 1 NLAERKRLVAQHLTHVSQTQEONKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240  
 2 NLAERKRLVAHDLTHVSQTQEONKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240  
 3 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240  
 4 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240  
 5 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240  
 6 NLTERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDKGITSEK 240  
 7 NLEERKRLVAQFLAESSQRS-QEASQREFSADPVIKSKTSQKYMALVNWLVEHGITSEK 236  
 C NL+ERKRLVA\*+L\*\*\*SQ\*\*\*Q\*\*\*\*+\*\*\*S\*\*PVI\*SKTS\*\*YM\*LV\*WLV\*+GITSEK  
 250 260 270 280 290 300  
 1 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPADIKTNRIYR 300  
 2 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPADIKTNRIYR 300  
 3 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ 300  
 4 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ 300  
 5 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPEDISSNRIYR 300  
 6 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQNPVEDISSNRIYK 300  
 7 QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKNIWQ 296  
 C QWIQE\*Q\*SY\*SFN\*\*\*NSRSQIKAALDNA:KIM+LTK:A\*DYLVG::\*\*+DI::NRI\*:  
 310 320 330 340 350 360  
 1 ILELNGYEPAYAGSVFLGWAQKRFGRNTIWLFGPATGKTNIAEATAHAVPFYGCNVNT 360  
 2 ILELNGYDPAYAGSVFLGWAQKRFGRNTIWLFGPATGKTNIAEATAHAVPFYGCNVNT 360  
 3 ILELNGYDPQYAASVFLGWAQKKFGRNTIWLFGPATGKTNIAEATAHAVPFYGCNVNT 360  
 4 ILELNGYDPQYAASVFLGWAQKKFGRNTIWLFGPATGKTNIAEATAHAVPFYGCNVNT 360  
 5 ILEMNGYDPQYAASVFLGWAQKKFGRNTIWLFGPATGKTNIAEATAHAVPFYGCNVNT 360  
 6 ILELNGYDPQYAASVFLGWATKKFGRNTIWLFGPATGKTNIAEATAHTVPFYGCNVNT 360  
 7 IFEMNGYDPAYAGSILYGWCQRSFNKRNVTWLVGPATGKTNIAEATAHTVPFYGCNVNT 356  
 C I+E+NGY\*P:YA:S\*\*\*GW\*\*\*:F\*KRNT\*WL\*GPATGKTNIAEATAH+VPFYGCNVNT

FIG. 3A

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      370      380      390      400      410      420
1  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIDPTPVIVTS 420
2  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIDPTPVIVTS 420
3  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIEPTPVIVTS 420
4  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIEPTPVIVTS 420
5  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIDPTPVIVTS 420
6  NENFPFND CVDK MVIWEEGKMTAKV VESAKAILGGSKVRVDQCKSSAQIDPTPVIVTS 420
7  NENFPFND CVDK MLIWEEGKMTNKV VESAKAILGGSKVRVDQCKSSVQIDSTPVIVTS 416
C  NENFPFND CVDK M*IWEEGKMT*KV VESAKAILGGSKVRVDQCKSS*QI+*TPVIVTS
      430      440      450      460      470      480
1  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL EHD F GKVT KQEVKEFFRWAQDHVTEV 480
2  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL EHD F GKVT KQEVKEFFRWAQDHVTEV 480
3  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL DHD F GKVT KQEVK DFFRWASDHVTDV 480
4  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL DHD F GKVT KQEVK DFFRWASDHVTDV 480
5  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL EHD F GKVT KQEVK DFFRWASDHVTEV 480
6  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRL DHD F GKVT KQEVK DFFRWAKDHVVEV 480
7  NTNMC VVDGNSTTFEHQQPLEDRMFKFELTKRL PPDFGKITKQEVK DFFAWAKVNQVPV 476
C  NTNMC *V*DGNSTTFEHQQPL*DRMFKFELT+RL: *DFGK*TKQEVK+FF*WA: ***+:V

      490      500      510      520
1  AHEFYVRKGGANKRPAPDDADKSEPKRA-----CPSVADPSTSDAEG 522
2  AHEFYVRKGGANKRPAPDDADKSEPKRA-----CPSVADPSTSDAEG 522
3  AHEFYVRKGGAKKRPA SNDADVSEPKRQ-----CTSLAQPTTSDAEA 522
4  AHEFYVRKGGAKKRPA SNDADVSEPKRQ-----CTSLAQPTTSDAEA 522
5  THEFYVRKGGARKRPAPNDADISEPKRA-----CPSVAQPSTSDAEA 522
6  EHEFYVKKGGAKKRPA PSDADISEPKRV-----RESVAQPSTSDAEA 522
7  THEFKVPRELAGTKGA EKSLKRPLGDVTNTSYKSLEKRARLSFVPETPRSSDVTVD PAPL 536
C  :HEF*V+***A:***A: :***.*****:
      530      540      550      560      570      580
1  APVDFADRYQNKCSRHAGMLQMLFPCKTCER MNQNFN ICFTHGTRDCSECFP--GVSESQ 580
2  APVDFADRYQNKCSRHAGMLQMLFPCKTCER MNQNFN ICFTHGTRDCSECFP--GVSESQ 580
3  P-ADYADRYQNKCSRHVGMNLMLFPCKTCER MNQI S NVC FTHGQRDCGECFPGMSESQPV 581
4  P-ADYADRYQNKCSRHVGMNLMLFPCKTCER MNQI S NVC FTHGQRDCGECFPGMSESQPV 581
5  P-VDYADRYQNKCSRHVGMNLMLFP CRQCER MNQNV D ICFTHGVMDCAECFP--VSESQPV 580
6  S-INYADRYQNKCSRHVGMNLMLFP CRQCER MNQNS N ICFTHGQKDCLECFP--VSESQPV 579
7  RPLNWN SRYDCKCDYHAQFDNISNKCDECEYLNRGKNGCICHNVTHCQICHG----- 588
C  ::+:**RY**KC**H:**:****C::CE**N*::*:C**H*:*C.*C**...+:::

      590      600      610      620
1  PVVRKR TYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ 623
2  PVVRKR TYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ 623
3  SVVKKK TYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ 624
4  SVVKKK TYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ 624
5  SVVRKR TYQKLCPIHHIMGRAPEVACSACELANVDLDDCDMEQ 623
6  VSVVKK AYQKLCYIHHIMG-KVPDACTACDLVNVDLDDCIFEQ 621
7  -----IPWEKENLSDFGDFDDANKEQ 610
C  :+*:*+*:*:*:*:*:*:*:*+*+*+*:*+*+*+*:*D*DD*: :EQ

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FIG. 3B